

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 08/910,449A
Source: IFW/6
Date Processed by STIC: 8/11/06

ENTERED



IFW16

RAW SEQUENCE LISTING DATE: 08/11/2006
PATENT APPLICATION: US/08/910,449A **TIME:** 09:40:45

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3 <110> APPLICANT: Goodwin, Raymond G.
4 Smith, Craig A.
6 <120> TITLE OF INVENTION: 4-1BB Polypeptides and DNA Encoding 4-1BB Polypeptides
8 <130> FILE REFERENCE: 2801-C
10 <140> CURRENT APPLICATION NUMBER: US 08/910,449A
11 <141> CURRENT FILING DATE: 1997-08-05
13 <150> PRIOR APPLICATION NUMBER: US 08/236,918
14 <151> PRIOR FILING DATE: 1994-05-06
16 <150> PRIOR APPLICATION NUMBER: US 08/060,843
17 <151> PRIOR FILING DATE: 1993-05-07
19 <160> NUMBER OF SEQ ID NOS: 17
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1254
25 <212> TYPE: DNA
26 <213> ORGANISM: Mus sp.
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (53)..(979)
32 <223> OTHER INFORMATION: (Clone: murine 4-1BB-L)
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41 5 10 15
43 ggt act tcg tgc ccc tcg gat gcg gcg ctc ctc aga gat acc ggg ctc 154
44 Gly Thr Ser Cys Pro Ser Asp Ala Ala Leu Leu Arg Asp Thr Gly Leu
45 20 25 30
47 ctc gcg gac gct gcg ctc tca gat act gtg cgc ccc aca aat gcc 202
48 Leu Ala Asp Ala Ala Leu Leu Ser Asp Thr Val Arg Pro Thr Asn Ala
49 35 40 45 50
51 gcg ctc ccc acg gat gct gcc tac cct gcg gtt aat gtt cgg gat cgc 250
52 Ala Leu Pro Thr Asp Ala Ala Tyr Pro Ala Val Asn Val Arg Asp Arg
53 55 60 65
55 gag gcc gcg tgg ccg cct gca ctg aac ttc tgt tcc cgc cac cca aag 298
56 Glu Ala Ala Trp Pro Pro Ala Leu Asn Phe Cys Ser Arg His Pro Lys
57 70 75 80
59 ctc tat ggc cta gtc gct ttg gtt ttg ctg ctt ctg atc gcc gcc tgt 346
60 Leu Tyr Gly Leu Val Ala Leu Val Leu Leu Leu Ile Ala Ala Cys
61 85 90 95
63 gtt cct atc ttc acc cgc acc gag cct cgg cca gcg ctc aca atc acc 394

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65	100			105				110									
67	acc	tgc	ccc	aac	ctg	ggt	acc	cga	gag	aat	aat	gca	gac	cag	gtc	acc	442
68	Thr	Ser	Pro	Asn	Leu	Gly	Thr	Arg	Glu	Asn	Asn	Ala	Asp	Gln	Val	Thr	
69	115				120				125							130	
71	cct	gtt	tcc	cac	att	ggc	tgc	ccc	aac	act	aca	caa	cag	ggc	tct	cct	490
72	Pro	Val	Ser	His	Ile	Gly	Cys	Pro	Asn	Thr	Thr	Gln	Gln	Gly	Ser	Pro	
73					135				140							145	
75	gtg	ttc	gcc	aag	cta	ctg	gct	aaa	aac	caa	gca	tcg	ttg	tgc	aat	aca	538
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79	act	ctg	aac	tgg	cac	agc	caa	gat	gga	gct	ggg	agc	tca	tac	cta	tct	586
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81					165				170							175	
83	caa	ggt	ctg	agg	tac	gaa	gaa	gac	aaa	aag	gag	ttg	tgc	gta	gac	agt	634
84	Gln	Gly	Leu	Arg	Tyr	Glu	Glu	Asp	Lys	Lys	Glu	Leu	Val	Val	Asp	Ser	
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87	ccc	ggg	ctc	tac	tac	gta	ttt	ttg	gaa	ctg	aag	ctc	agt	cca	aca	ttc	682
88	Pro	Gly	Leu	Tyr	Tyr	Val	Phe	Leu	Glu	Leu	Lys	Leu	Ser	Pro	Thr	Phe	
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91	aca	aac	aca	ggc	cac	aag	gtg	cag	ggc	tgg	gtc	tct	ctt	gtt	ttg	caa	730
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93					215				220							225	
95	gca	aag	cct	cag	gta	gat	gac	ttt	gac	aac	ttg	gcc	ctg	aca	gtg	gaa	778
96	Ala	Lys	Pro	Gln	Val	Asp	Asp	Phe	Asp	Asn	Leu	Ala	Leu	Thr	Val	Glu	
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99	ctg	ttc	cct	tgc	tcc	atg	gag	aac	aag	tta	gtg	gac	cgt	tcc	tgg	agt	826
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103	caa	ctg	ttg	ctc	ctg	aag	gct	ggc	cac	cgc	ctc	agt	gtg	ggt	ctg	agg	874
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107	gct	tat	ctg	cat	gga	gcc	cag	gat	gca	tac	aga	gac	tgg	gag	ctg	tct	922
108	Ala	Tyr	Leu	His	Gly	Ala	Gln	Asp	Ala	Tyr	Arg	Asp	Trp	Glu	Leu	Ser	
109					275				280							285	290
111	tat	ccc	aac	acc	acc	agc	ttt	gga	ctc	ttt	ctt	gtg	aaa	ccc	gac	aac	970
112	Tyr	Pro	Asn	Thr	Thr	Ser	Phe	Gly	Leu	Phe	Leu	Val	Lys	Pro	Asp	Asn	
113					295				300							305	
115	cca	tgg	gaa	tgagaactat	ccttcttgcgt	actccttagtt	gctaaatgttt										1019
116	Pro	Trp	Glu														
119	caagctgcta	tgttttatgg	ggtctgagca	ggggccctt	ccatgacttt	ctcttgtctt											1079
121	taactggact	tggattttat	tctgagcata	gctcagacaa	gactttatat	aattcactag											1139
123	atagcattag	taaactgctg	ggcagctgct	agataaaaaaa	aaatttctaa	atcaaagttt											1199
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136 1 5 10 15
139 Pro Ala Gly Thr Ser Cys Pro Ser Asp Ala Ala Leu Leu Arg Asp Thr
140 20 25 30
143 Gly Leu Leu Ala Asp Ala Ala Leu Leu Ser Asp Thr Val Arg Pro Thr
144 35 40 45
147 Asn Ala Ala Leu Pro Thr Asp Ala Ala Tyr Pro Ala Val Asn Val Arg
148 50 55 60
151 Asp Arg Glu Ala Ala Trp Pro Pro Ala Leu Asn Phe Cys Ser Arg His
152 65 70 75 80
155 Pro Lys Leu Tyr Gly Leu Val Ala Leu Val Leu Leu Leu Ile Ala
156 85 90 95
159 Ala Cys Val Pro Ile Phe Thr Arg Thr Glu Pro Arg Pro Ala Leu Thr
160 100 105 110
163 Ile Thr Thr Ser Pro Asn Leu Gly Thr Arg Glu Asn Asn Ala Asp Gln
164 115 120 125
167 Val Thr Pro Val Ser His Ile Gly Cys Pro Asn Thr Thr Gln Gln Gly
168 130 135 140
171 Ser Pro Val Phe Ala Lys Leu Leu Ala Lys Asn Gln Ala Ser Leu Cys
172 145 150 155 160
175 Asn Thr Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser Tyr
176 165 170 175
179 Leu Ser Gln Gly Leu Arg Tyr Glu Glu Asp Lys Lys Glu Leu Val Val
180 180 185 190
183 Asp Ser Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser Pro
184 195 200 205
187 Thr Phe Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu Val
188 210 215 220
191 Leu Gln Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu Thr
192 225 230 235 240
195 Val Glu Leu Phe Pro Cys Ser Met Glu Asn Lys Leu Val Asp Arg Ser
196 245 250 255
199 Trp Ser Gln Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val Gly
200 260 265 270
203 Leu Arg Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu
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216 <211> LENGTH: 1618
217 <212> TYPE: DNA
218 <213> ORGANISM: Homo sapiens
221 <220> FEATURE:
222 <221> NAME/KEY: CDS
223 <222> LOCATION: (4)..(765)
224 <223> OTHER INFORMATION: (clone: human 4-1BB-L (7A))
226 <400> SEQUENCE: 3

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231	cct	ccc	gcg	ccc	cgc	gct	cgc	gcc	tgc	cgc	gta	ctg	cct	tgg	gcc	ctg	96	
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235	gtc	gcg	ggg	ctg	ctg	ctg	ctg	ctg	ctc	gct	gcc	gcc	tgc	gcc	gtc	144		
236	Val	Ala	Gly	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Ala	Ala	Cys	Ala	Val		
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239	ttc	ctc	gcc	tgc	ccc	tgg	gcc	gtg	tcc	ggg	gct	cgc	gcc	tcg	ccc	ggc	192	
240	Phe	Leu	Ala	Cys	Pro	Trp	Ala	Val	Ser	Gly	Ala	Arg	Ala	Ser	Pro	Gly		
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243	tcc	gcg	gcc	agc	ccg	aga	ctc	cgc	gag	ggt	ccc	gag	ctt	tcg	ccc	gac	240	
244	Ser	Ala	Ala	Ser	Pro	Arg	Leu	Arg	Glu	Gly	Pro	Glu	Leu	Ser	Pro	Asp		
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247	gat	ccc	gcc	ggc	ctc	ttg	gac	ctg	cg	cag	ggc	atg	ttt	g	cg	cag	ctg	288
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260	Glu	Asp	Thr	Lys	Glu	Leu	Val	Val	Ala	Lys	Ala	Gly	Val	Tyr	Tyr	Val		
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263	tcc	ttt	caa	cta	gag	ctg	cgg	cgc	gtg	gtg	gcc	ggc	gag	ggc	tca	ggc	480	
264	Phe	Phe	Gln	Leu	Glu	Leu	Arg	Arg	Val	Val	Ala	Gly	Glu	Gly	Ser	Gly		
265						145			150							155		
267	tcc	gtt	tca	ctt	g	cg	ctg	cac	ctg	cag	cca	ctg	cgc	tct	g	ct	528	
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275	gct	cgg	aac	tcg	gcc	tcc	ggt	ttc	cag	ggc	cgc	ttg	ctg	cac	ctg	agt	624	
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280	Ala	Gly	Gln	Arg	Leu	Gly	Val	His	Leu	His	Thr	Glu	Ala	Arg	Ala	Arg		
281						210			215							220		
283	cat	gcc	tgg	cag	ctt	acc	cag	ggc	gcc	aca	gtc	ttt	gga	ctc	ttc	cg	720	
284	His	Ala	Trp	Gln	Leu	Thr	Gln	Gly	Ala	Thr	Val	Leu	Gly	Leu	Phe	Arg		
285						225			230							235		
287	gtg	acc	ccc	gaa	atc	cca	gcc	gga	ctc	cct	tca	ccg	agg	tcg	gaa		765	
288	Val	Thr	Pro	Glu	Ile	Pro	Ala	Gly	Leu	Pro	Ser	Pro	Arg	Ser	Glu			
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297	atatttattc	tgagccctgag	ctcagataat	atattatata	tattatatat	atatatata	1005										
299	ttcttattaa	agaggatcct	gagtttgta	atggactttt	ttagaggagt	tgttttgggg	1065										
301	ggggggctt	cgacattgcc	gaggctggtc	ttgaactcct	ggacttagac	gatccctcctg	1125										
303	cctcagcctc	ccaagcaact	gggattcatc	ctttctatta	attcattgtta	cttatttgcc	1185										
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307	gaaacatcta	gaaatagact	gaaagaaaat	ctgagttatg	gtaatacgtg	aggaatttaa	1305										
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313	agtcaatgca	gcctccagcc	tcgacctccc	gaggctcagg	tgatcctccc	atctcagcct	1485										
315	ctcgagtagc	tgggaccaca	gttgtgtgcc	accacactt	gctaactttt	taatttttt	1545										
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337	Ala	Gly	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Ala	Ala	Cys	Ala	Val	Phe		
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341	Leu	Ala	Cys	Pro	Trp	Ala	Val	Ser	Gly	Ala	Arg	Ala	Ser	Pro	Gly	Ser	
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345	Ala	Ala	Ser	Pro	Arg	Leu	Arg	Glu	Gly	Pro	Glu	Leu	Ser	Pro	Asp	Asp	
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358						115				120					125		
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362						130				135					140		
365	Phe	Gln	Leu	Glu	Leu	Arg	Arg	Val	Val	Ala	Gly	Glu	Gly	Ser	Gly	Ser	
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369	Val	Ser	Leu	Ala	Leu	His	Leu	Gln	Pro	Leu	Arg	Ser	Ala	Ala	Gly	Ala	
370							165				170				175		
373	Ala	Ala	Leu	Ala	Leu	Thr	Val	Asp	Leu	Pro	Pro	Ala	Ser	Ser	Glu	Ala	
374						180				185					190		
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VERIFICATION SUMMARY

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